us-10-007-047-1.rni

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 02:15:21 ; Search time 689 Seconds
                                  (without alignments)
                                  10767.603 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 4534
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Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES

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1	3855	85.0	6628	4	US-09-949-016-4586	Sequence 4586, Ap
2	3754.8	82.8	4796	3	US-09-085-199B-3	Sequence 3, Appli
3	1664.4	36.7	2301	3	US-09-085-199B-8	Sequence 8, Appli
4	1155.2	25.5	1164	3	US-09-085-199B-1	Sequence 1, Appli
5	1118.4	24.7	3715	3	US-09-085-199B-44	Sequence 44, Appl
6	1116.8	24.6	68702	4	US-09-949-016-16328	Sequence 16328, A
7	970	21.4	3979	3	US-09-085-199B-10	Sequence 10, Appl
8	715.4	15.8	3876	4	US-09-849-602-4	Sequence 4, Appli
9	483.2	10.7	3251	3	US-09-085-199B-6	Sequence 6, Appli
10	187	4.1	436	3	US-09-085-199B-28	Sequence 28, Appl
c 11	187	4.1	601	4	US-09-949-016-163605	Sequence 163605,
12	175.4	3.9	279	3	US-09-085-199B-43	Sequence 43, Appl
13	149	3.3	485	3	US-09-085-199B-32	Sequence 32, Appl
14	147.2	3.2	193	3	US-09-085-199B-17	Sequence 17, Appl
15	144.6	3.2	578	3	US-09-085-199B-25	Sequence 25, Appl
16	144	3.2	565	3	US-09-085-199B-23	Sequence 23, Appl
17	138.8	3.1	498	3	US-09-085-199B-36	Sequence 36, Appl

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	19	126.6	2.8	418	3	US-09-085-199B-42	Sequence 42, Appl
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	21	125	2.8	359	3	US-09-085-199B-30	Sequence 30, Appl
c	22	116	2.6	510	4	US-09-270-767-928	Sequence 928, App
c	23	116	2.6	510	4	US-09-270-767-16210	Sequence 16210, A
	24	114	2.5	427	3	US-09-085-199B-37	Sequence 37, Appl
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	44	80.4	1.8	327	3	US-09-085-199B-20	Sequence 20, Appl
	45	79.8	1.8	3489	2	US-08-728-323A-1	Sequence 1, Appli

RESULT 8
US-09-849-602-4
; Sequence 4, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3876
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-602-4

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  Matches 1458;  Conservative    0;  Mismatches 1006;  Indels   99;  Gaps    4;

Qy      619 ATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGTATTCAACTCCCTGGAC 678
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Db       61 ACGGCCATCGCCGTATCCCAGATGTCCTCAGGCCAGTGCCGCCTGGCCCCCCTCATCCAG 120
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Qy    739 GTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCTTCTCTTCAAACTCCAC 798
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Db    241 AGCCTCAGGAACTTCTTCCGCAGAGCCTCCGACATGCTGTACTTCAAGCGGCTCATCCAG 300

Qy    919 ATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTCAGCCCTGTCAGAACAT 978
          |||||||| ||||||| |||  || || ||||||||||||| |||||||||||||| | || ||
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Qy   1099 GATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTTCAACAGTCAAAATGGT 1158
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Qy   1279 CACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCTGCGGCAGCAGGCGGCC 1338
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Qy   1339 GACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAGGCAGCGGGAGGACACC 1398
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Qy   1399 GAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCAAGCCAATGAACAGCGA 1458
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Db    745 GAGCGGAGCCAGGGCCTGCGTGAGGAGGCTGAGAGGAAGGCCAGTGCCACGGAGGCGCGC 804

Qy   1459 TATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCACGCTGACCTGCTGCGG 1518
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Qy   1519 AAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGCCCAGGTAGATTTGGAA 1578
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Qy   1639 ACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACTTGCCACAAGCCAACGG 1698
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Qy   1699 GAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTCAGAAGCAAACTGGGCA 1758
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Qy   1759 GCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAGTGGCGCAGCTCATAGG 1818
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Qy   1819 GAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCAGCTCAAACTGGCCAGC 1878
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Qy   1879 ACAGAG----------------------GAATCTATGTGCCAGCTTGCCAAAGACCAA 1914
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Db   1225 GAGCAGCAGCGCAGCTCCCAGGAGCAGGGCGAGTTGCAGGGCCGGCTGGCAGAGAGGGAG 1284

Qy   1915 CGAAAAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAG------------------ 1956
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Qy   1957 --------------------GTGATACAAGACGCCCTGAACCAGCTTGAAGAACCTCCT 1995
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Db   1345 GCTGCTGCCGAGGCCGCGGGCATCCTGCAGGATGCCGTGAGCAAGCTGGACGACCCCCTG 1404

Qy   1996 CTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCACATCCATTTCCAGC 2055
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Db   1405 CACCTGCGCTGTACCAGCTCCCCAGACTACCTGGTGAGCAGGGCCCAGGAGGCCTTGGAT 1464

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Qy   2116 GGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGT 2175
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Qy   2236 CAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGAGGGAAGCCTTGAG 2295
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Db   1645 GAGTGCGGGGCCCGGGCTCTGGAGCTCATGGGGCAGCTGCAGGACCAGCAGGCTCTGCGG 1704

Qy   2296 AATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAG 2355
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Db   1705 CACATGCAGGCCAGCCTGGTGCGGACACCCCTGCAGGGCATCCTTCAGCTGGGCCAGGAA 1764

Qy   2356 CTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAG 2415
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Qy   2536 TGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGA 2595
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Db   1945  TGCACAGACCTGATGAAGGCTATCCGGCTCCTGGTGACGACATCCACTAGCCTGCAGAAG 2004

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Qy   2656  CGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATG 2715
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Db   2245  AAGCACAGCCCCCACCTGAGCCGCCTGCAGGAATGTTCTCGCACAGTCAATGAGAGGGCT 2304

Qy   2896  GCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGAGACAGACAACATG 2955
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